

SEQUENCE LISTING

<110> Jing, Shuqian

<120> IL-17 Receptor Like Molecules and Uses Thereof

<130> 01017/39525

<140> To be assigned

<141> Herewith

<150> 09/809,567

<151> 2001-03-15

<150> 09/724,460

<151> 2000-11-28

<150> 60/189,816

<151> 2000-03-16

<160> 19

<170> PatentIn Ver. 2.0

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<211> 3083

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (22)..(2235)

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Phe	Phe	Thr	Val	Asn	Ala	Cys	Leu	Asn	Gly	Ser	Gln	Leu	Ala	Val	Ala	
			15					20					25			
gct	ggc	ggg	tcc	ggc	cgc	gcg	tgg	ggc	gtc	gac	acc	tgt	ggc	tgg	agg	147
Ala	Gly	Gly	Ser	Gly	Arg	Ala	Trp	Gly	Val	Asp	Thr	Cys	Gly	Trp	Arg	
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Gly	Val	Gly	Pro	Ala	Ser	Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	
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Lys	Tyr	Asp	Asn	Cys	Thr	Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	
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att	gct	gac	gcc	cag	aat	atc	acc	atc	agc	cag	tat	gct	tgc	cat	gac	291
Ile	Ala	Asp	Ala	Gln	Asn	Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	
	75					80				85					90	
caa	gtg	gca	gtc	acc	att	ctt	tgg	tcc	cca	ggg	gcc	ctc	ggc	atc	gaa	339
Gln	Val	Ala	Val	Thr	Ile	Leu	Trp	Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	
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Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly	
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Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser	
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Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys	
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Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys	
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Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp	
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Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro	
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Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe	
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Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr	
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Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu	
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Gln Thr Thr Glu Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly	
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Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile	
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Arg Ala Met Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala	
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Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr	
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Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg	
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Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala	
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Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys	
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Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr
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gat gaa ctc cac gcg gtc gcc cct ttgtaacaaa acgaaagagt ctaagcattg 2265
Asp Glu Leu His Ala Val Ala Pro
735

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ttggagctga ggtotcatc aaggatattt ggagtgaat gctggccagt acttggtctc 2385

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 <213> Homo sapiens

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Ala	Trp	Gly	Val	Asp	Thr	Cys	Gly	Trp	Arg	Gly	Val	Gly	Pro	Ala	Ser
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Arg	Asn	Ser	Gly	Leu	Tyr	Asn	Ile	Thr	Phe	Lys	Tyr	Asp	Asn	Cys	Thr
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Thr	Tyr	Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala	Gln	Asn
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Ile	Thr	Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile
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Val	Ile	Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Cys	Gln	Gln	Leu
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Val	Lys	Val	Val	Pro	Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His
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Pro	Phe	Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Leu	Gln	Pro	Asp
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Ser	Cys	Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	Leu
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Val	Asp	Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	Lys
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Pro	Val	His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Met	Ala	Ile	Thr
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Val	Pro	Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val	Met	305	310	315	320
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Ser	Ser	Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg	Leu	340	345	350	
Arg	Pro	Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly	Gln	355	360	365	
Asn	His	Met	Asn	Val	Val	Gln	Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp	Phe	370	375	380	
Cys	Gly	Cys	Glu	Val	Ala	Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu	Cys	385	390	395	400
Arg	Glu	Gly	Gln	Arg	Glu	Trp	Val	Ile	Gln	Lys	Ile	His	Glu	Ser	Gln	405	410	415	
Phe	Ile	Ile	Val	Val	Cys	Ser	Lys	Gly	Met	Lys	Tyr	Phe	Val	Asp	Lys	420	425	430	
Lys	Asn	Tyr	Lys	His	Lys	Gly	Gly	Gly	Arg	Gly	Ser	Gly	Lys	Gly	Glu	435	440	445	
Leu	Phe	Leu	Val	Ala	Val	Ser	Ala	Ile	Ala	Glu	Lys	Leu	Arg	Gln	Ala	450	455	460	
Lys	Gln	Ser	Ser	Ser	Ala	Ala	Leu	Ser	Lys	Phe	Ile	Ala	Val	Tyr	Phe	465	470	475	480
Asp	Tyr	Ser	Cys	Glu	Gly	Asp	Val	Pro	Gly	Ile	Leu	Asp	Leu	Ser	Thr	485	490	495	
Lys	Tyr	Arg	Leu	Met	Asp	Asn	Leu	Pro	Gln	Leu	Cys	Ser	His	Leu	His	500	505	510	
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Ser	Arg	Arg	Asn	Tyr	Phe	Arg	Ser	Lys	Ser	Gly	Arg	Ser	Leu	Tyr	Val	530	535	540	
Ala	Ile	Cys	Asn	Met	His	Gln	Phe	Ile	Asp	Glu	Glu	Pro	Asp	Trp	Phe	545	550	555	560
Glu	Lys	Gln	Phe	Val	Pro	Phe	His	Pro	Pro	Pro	Leu	Arg	Tyr	Arg	Glu	565	570	575	
Pro	Val	Leu	Glu	Lys	Phe	Asp	Ser	Gly	Leu	Val	Leu	Asn	Asp	Val	Met	580	585	590	
Cys	Lys	Pro	Gly	Pro	Glu	Ser	Asp	Phe	Cys	Leu	Lys	Val	Glu	Ala	Pro	595	600	605	
Val	Leu	Gly	Ala	Thr	Gly	Pro	Ala	Asp	Ser	Gln	His	Glu	Ser	Gln	His	610	615	620	
Gly	Gly	Leu	Asp	Gln	Asp	Gly	Glu	Ala	Arg	Pro	Ala	Leu	Asp	Gly	Ser	625	630	635	640

Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
645 650 655

Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
660 665 670

Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
675 680 685

Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu
690 695 700

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Ala Pro

<210> 3

<211> 810

<212> PRT

<213> Homo sapiens

<400> 3

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35 40 45

Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
50 55 60

Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
65 70 75 80

His Phe Ala His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
85 90 95

Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
100 105 110

Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
115 120 125

Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Arg Trp Arg Phe
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Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Glu Tyr Glu Val Thr
145 150 155 160

Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln
165 170 175

Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val
180 185 190

Thr	Thr	Pro	Cys	Met	Ser	Ser	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	195	200	205
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Glu	Asn	His	Ser	Cys	Phe	Glu	His	Met	His	His	Ile	Pro	Ala	Pro	Arg	245	250	255
Pro	Glu	Glu	Phe	His	Gln	Arg	Ser	Asn	Val	Thr	Leu	Thr	Leu	Arg	Asn	260	265	270
Leu	Lys	Gly	Cys	Cys	Arg	His	Gln	Val	Gln	Ile	Gln	Pro	Phe	Phe	Ser	275	280	285
Ser	Cys	Leu	Asn	Asp	Cys	Leu	Arg	His	Ser	Ala	Thr	Val	Ser	Cys	Pro	290	295	300
Glu	Met	Pro	Asp	Thr	Pro	Glu	Pro	Ile	Pro	Asp	Tyr	Met	Pro	Leu	Trp	305	310	315
Val	Tyr	Trp	Phe	Ile	Thr	Gly	Ile	Ser	Ile	Leu	Leu	Val	Gly	Ser	Val	325	330	335
Ile	Leu	Leu	Ile	Val	Cys	Met	Thr	Trp	Arg	Leu	Ala	Gly	Pro	Gly	Ser	340	345	350
Glu	Lys	Tyr	Ser	Asp	Asp	Thr	Lys	Tyr	Thr	Asp	Gly	Leu	Pro	Ala	Ala	355	360	365
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Ser	Ala	Asp	His	Pro	Leu	Tyr	Val	Asp	Val	Val	Leu	Lys	Phe	Ala	Gln	385	390	395
Phe	Leu	Leu	Thr	Ala	Cys	Gly	Thr	Glu	Val	Ala	Leu	Asp	Leu	Leu	Glu	405	410	415
Glu	Gln	Ala	Ile	Ser	Glu	Ala	Gly	Val	Met	Thr	Trp	Val	Gly	Arg	Gln	420	425	430
Lys	Gln	Glu	Met	Val	Glu	Ser	Asn	Ser	Lys	Ile	Ile	Val	Leu	Cys	Ser	435	440	445
Arg	Gly	Thr	Arg	Ala	Lys	Trp	Gln	Ala	Leu	Leu	Gly	Arg	Gly	Ala	Pro	450	455	460
Val	Arg	Leu	Arg	Cys	Asp	His	Gly	Lys	Pro	Val	Gly	Asp	Leu	Phe	Thr	465	470	475
Ala	Ala	Met	Asn	Met	Ile	Leu	Pro	Asp	Phe	Lys	Arg	Pro	Ala	Cys	Phe	485	490	495
Gly	Thr	Tyr	Val	Val	Cys	Tyr	Phe	Ser	Glu	Val	Ser	Cys	Asp	Gly	Asp	500	505	510
Val	Pro	Asp	Leu	Phe	Gly	Ala	Ala	Pro	Arg	Tyr	Pro	Leu	Met	Asp	Arg	515	520	525

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 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp
 565 570 575
 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser
 580 585 590
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu
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 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly
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 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala
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 675 680 685
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 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Ser Thr Pro Met Ala Ser
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 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met
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 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu
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<223> Description of Artificial Sequence: Primer 2417-51

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<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer 1916-83

<400> 7
 ggctcgtatg ttgtgtggaa ttgtgagcg 29

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer 2418-63

<400> 8
 cgagccatgc tggctgatgt tc 22

<210> 9
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Primer 1916-82

<400> 9
 gattacgcca agctctaata cgactc 26

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2432-38

<400> 10
gaagctactg ttgagctgct tcg

23

<210> 11
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2432-36

<400> 11
ccgatccagc ctccggactc tag

23

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2430-12

<400> 12
gcgtcagcaa tcacatgctt ccc

23

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2144-06

<400> 13
gcgtatttag gtgacactat agaac

25

<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2417-51

<400> 14
ccagtgtttc gcctacttcc tcc

23

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 2417-65

<400> 15
ggagcttttc ggcaatggct gac 23

<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 16
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Lys
1 5 10

<210> 17
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 17
Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg
1 5 10 15

Arg Arg

<210> 18
<211> 1723
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (75)..(959)

<400> 18
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gtgggggggcc atga agc ggg cag aaa gag agg tgg atg atg tcc ggg gac 110
Ser Gly Gln Lys Glu Arg Trp Met Met Ser Gly Asp
1 5 10

tgg cat gac cct ggg tca cag cag tgc tgc ttg cat ttg gac tcc atg 158
Trp His Asp Pro Gly Ser Gln Gln Cys Cys Leu His Leu Asp Ser Met
15 20 25

ggg ctt tgt gtt gga aga gca aat tgg ctt cac tct gca tca tgt tct 206
Gly Leu Cys Val Gly Arg Ala Asn Trp Leu His Ser Ala Ser Cys Ser
30 35 40

ctt gtt ttc cca cag gga gtg ggg cca gcc agc aga aac agt ggg ctg	254
Leu Val Phe Pro Gln Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu	
45 50 55 60	
tac aac atc acc ttc aaa tat gac aat tgt acc acc tac ttg aat cca	302
Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro	
65 70 75	
gtg ggg aag cat gtg att gct gac gcc cag aat atc acc atc agc cag	350
Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln	
80 85 90	
tat gct tgc cat gac caa gtg gca gtc acc att ctt tgg tcc cca ggg	398
Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly	
95 100 105	
gcc ctc ggc atc gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag	446
Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu	
110 115 120	
ctg aag tcg gag gga aga cag tgc caa caa ctg att cta aag gat ccg	494
Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro	
125 130 135 140	
aag cag ctc aac agt agc ttc aaa aga act gga atg gaa tct caa cct	542
Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro	
145 150 155	
ttc ctg aat atg aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct	590
Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro	
160 165 170	
ttt cct tcc att aaa aac gaa agc aat tac cac cct ttc ttc ttt aga	638
Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg	
175 180 185	
acc cga gcc tgt gac ctg ttg tta cag ccg gac aat cta gct tgt aaa	686
Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys	
190 195 200	
ccc ttc tgg aag cct cgg aac ctg aac atc agc cag cat ggc tcg gac	734
Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp	
205 210 215 220	
atg cag gtg tcc ttc gac cac gca ccg cac aac ttc ggc ttc cgt ttc	782
Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe	
225 230 235	
ttc tat ctt cac tac aag ctc aag cac gaa gga cct ttc aag cga aag	830
Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys	
240 245 250	
acc tgt aag cag gag caa act aca gag atg acc agc tgc ctc ctt caa	878
Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser Cys Leu Leu Gln	
255 260 265	
aat gtt tct cca ggg gat tat ata att gag ctg gtg gat gac act aac	926
Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn	
270 275 280	
aca aca aga aaa gtg atg cat tat gcc tta aag cggggggctt gcaccctgc	979
Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys	
285 290 295	

tggaaagaaa aggtttgtgt atatttctga tgcaaagtgc ataactcactg ctctgtaaag 1039
 gcagctggca gctttttggg aaaagaacgt gctcgtctgt tctctggcat caagtttctt 1099
 gcagctgctc tgagggagag acagtgagct gcaagactgc ctccccataa caacaggcaa 1159
 ctcagagaag agtcatttta tgttggttct atggaatctg gaatgagtgc agagctccta 1219
 cccacacatg actgccccgc catttcatcc taggcattct gtgaaggaga ttggttagtc 1279
 caaacttgct aacatacgaa aattcacttg gaacatgatg agagatttct tattgaggcc 1339
 aagagatggt tctgtccca gaggaaccat taggagtgc ttttagggta ttcagctttg 1399
 ttcatgaaat aaggcatctc tgagaaagtg gccccaggga gagaatggag gactgggagg 1459
 agaagcatta actgagctcc aagggtgtgt gggcagagag cttgctatgt gaactcactc 1519
 cttaagaaaa tggaagagaa aaagagagtg ctagttaaaa aatcgggatg ttttagtttg 1579
 gatttaggggt tttgatactt atgttgaaat actaatgttt ctgatcaata aaatcaaact 1639
 cttaatatat cgagtaatga aaccatagtg tgattgcctc agaataaatt gagaagtcca 1699
 aaaaaaaaaa aaaaaaaaaa aaaa 1723

<210> 19
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 19
 Ser Gly Gln Lys Glu Arg Trp Met Met Ser Gly Asp Trp His Asp Pro
 1 5 10 15
 Gly Ser Gln Gln Cys Cys Leu His Leu Asp Ser Met Gly Leu Cys Val
 20 25 30
 Gly Arg Ala Asn Trp Leu His Ser Ala Ser Cys Ser Leu Val Phe Pro
 35 40 45
 Gln Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
 50 55 60
 Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
 65 70 75 80
 Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His
 85 90 95
 Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile
 100 105 110
 Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu
 115 120 125
 Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn
 130 135 140
 Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met
 145 150 155 160

Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile
165 170 175

Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe Arg Thr Arg Ala Cys
180 185 190

Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys
195 200 205

Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser
210 215 220

Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His
225 230 235 240

Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln
245 250 255

Glu Gln Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro
260 265 270

Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys
275 280 285

Val Met His Tyr Ala Leu Lys Pro
290 295